BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using <u>BLAST</u> engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program `blastp` Matrix `0 BLOSUM62`

Parameters used in <u>BLASTN</u> program only:

Reward for a match: [＿＿＿] **Penalty for a mismatch:** [＿＿＿]

Open gap `11` and extension gap `1` penalties

gap x_dropoff `50` expect `1000` word size `2` <u>Filter</u> ☐

Sequence 1 Enter accession or GI [＿＿＿]
or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

```
YTSALQP
```

Light chain CDR2

Murine 21.6

Sequence 2 Enter accession or GI [＿＿＿]
or sequence in FASTA format from: [＿＿＿] to: [＿＿＿]

```
GISNRFS
```

residues 75-81 of SEQ ID NO: 12

[Align] [Clear Input]

Comments and suggetstions to: <u>blast-help@ncbi.nlm.nih.gov</u>
Credits to: <u>Tatiana Tatusov</u> and <u>Tom Madden</u>

EXHIBIT

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix `0 BLOSUM62` gap open: `11` gap extension: `1`
x_dropoff: `50` expect: `1000` wordsize: `2` Filter ☐ `Align`

Sequence 1 lcl|seq_1 **Length 7**
Sequence 2 lcl|seq_2 **Length 7**
No siginificant similarity was found